

Diagram illustrating the centromeric region of chromosome 11p15.5, showing the centromeric side and telomeric side. The centromeric side is marked by a dashed line. The centromeric region is marked by a solid line. The telomeric side is marked by a dashed line. Key features include:

- Centromeric side (top):** yUP19H6L, m305, NPR1, yUP21A4L, g8020, yUP11H9L.
- Centromeric region (middle):** GAP-B, g4026, yUP19H6L, m305, yUP21A4L, g8020, yUP11H9L, g11447.
- Telomeric side (bottom):** m315.

Scale bars indicate 5kb and 2cM.

FIG. 2A

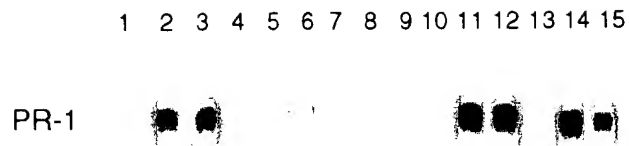


FIG. 2B

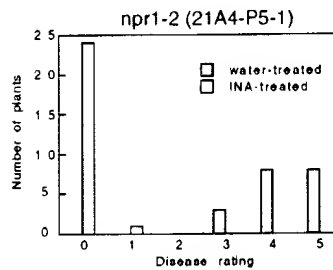
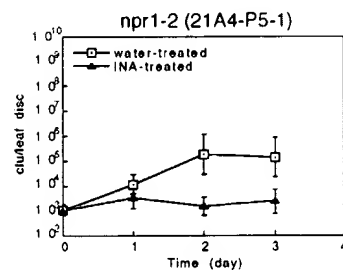
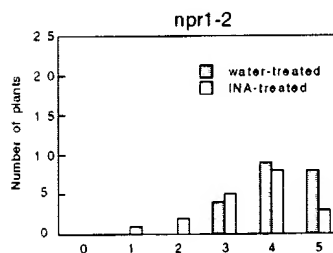
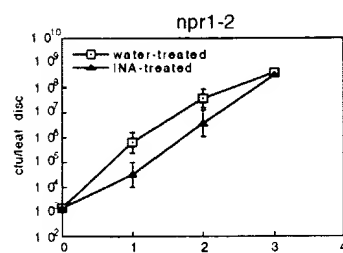
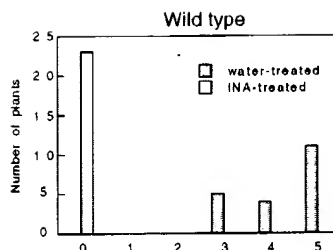
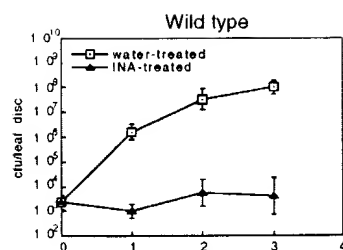
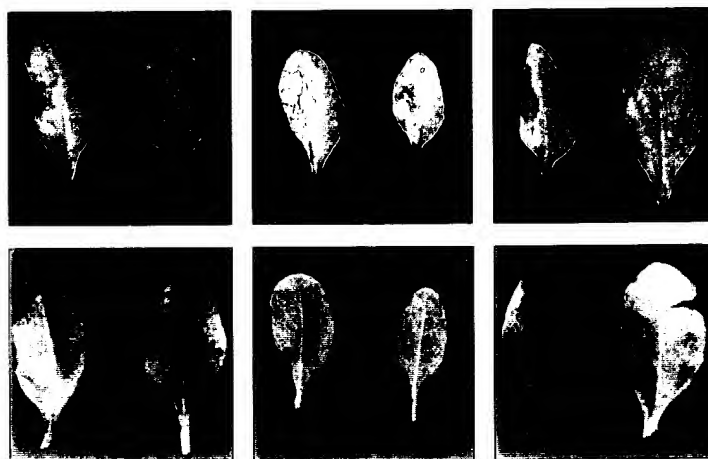


FIG. 2C

FIG. 2D

# Restriction Map of the *NPR1* Locus (7547 bp)

## Unique Sites

## Hind III and Xba I Sites

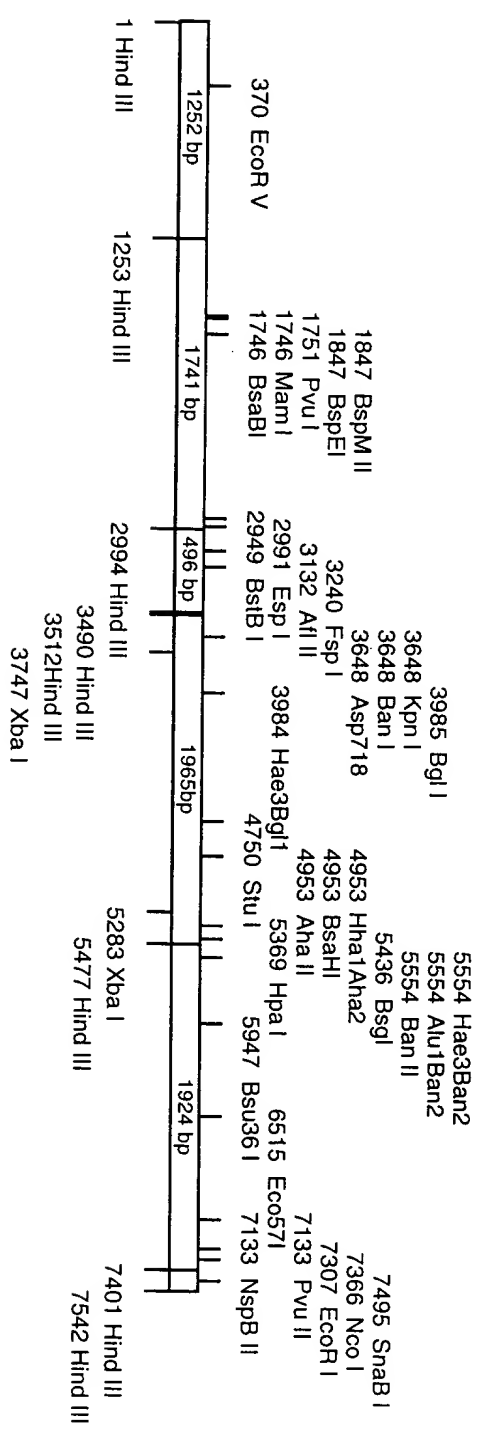


FIG. 3

10	20	30	40	50
*	*	*	*	*
AAGCTTGTGA	TGCAAGTCAT	GGGATATTGC	TTTGTGTTAA	GTATACAAAA
TTCGAACACT	ACGTTTCAGTA	CCCTATAACG	AAACACAATT	CATATGTTTT
60	70	80	90	100
*	*	*	*	*
CCATCACGTG	GATACATAGT	CTTCAAACCA	ACCACTAAAC	AGTATCAGGT
GGTAGTGCAC	CTATGTATCA	GAAGTTTGGT	TGGTGATTTG	TCATAGTCCA
110	120	130	140	150
*	*	*	*	*
CATACCAAAG	CCAGAAGTGA	AGGGTTGGGA	TATGTCATTG	GGTTTAGCGG
GTATGGTTTC	GGTCTTCACT	TCCCAACCCT	ATACAGTAAC	CCAAATCGCC
160	170	180	190	200
*	*	*	*	*
TAATCGGATT	GAACCCTTTC	CGGTATAAAA	TACAAAGGCT	TTCGCAGTCT
ATTAGCCTAA	CTTGGGAAAG	GCCATATTTT	ATGTTTCCGA	AAGCGTCAGA
210	220	230	240	250
*	*	*	*	*
CGGCGTATGT	GTATGTCTCG	GGGTATCTAC	CATTTGAATC	ACAGAACTTT
GCCGCATACA	CATACAGAGC	CCCATAGATG	GTAAACTTAG	TGTCTTGAAA
260	270	280	290	300
*	*	*	*	*
TATGTGCGAA	GTTTTTCGATT	CTGATTTCGTT	TACCTGGAAG	AGATTAGAAA
ATACACGCTT	CAAAAGCTAA	GACTAAGCAA	ATGGACCTTC	TCTAATCTTT
310	320	330	340	350
*	*	*	*	*
TTTGCGTCTA	CCAAAAACAG	ACAGATTAAT	TTTTTCCAAC	CCGATACAAG
AAACGCAGAT	GGTTTTTGTC	TGTCTAATTA	AAAAAGGTTG	GGCTATGTTC
360	370	380	390	400
*	*	*	*	*
TTTCGGGGTT	CTTGCATTGG	ATATCACGGA	ACAACAATGT	GATCCGGTTT
AAAGCCCCAA	GAACGTAACC	TATAGTGCCT	TGTTGTTACA	CTAGGCCAAA
410	420	430	440	450
*	*	*	*	*
TGTCTCAAAA	CCGAAACTTG	GTCCTTCTTC	CATACTCCGA	ACTCTGATGT
ACAGAGTTTT	GGCTTTGAAC	CAGGAAGAAG	GTATGAGGCT	TGAGACTACA
460	470	480	490	500
*	*	*	*	*
TTTCTCAGGA	TTAGTCAGAT	ACGAAGGGAA	GCTAGGTGCT	ATTCGTCAGT
AAAGAGTCCT	AATCAGTCTA	TGCTTCCCTT	CGATCCACGA	TAAGCAGTCA
510	520	530	540	550
*	*	*	*	*
GGACAAACAA	AGATCAAGAA	GATGTTACAG	AGTTATGGGT	TTTAAAGAGC

269884-0303

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CCTGTTTGTT TCTAGTTCTT CTACAAGTGC TCAATACCCA AAATTTCTCG

      560      570      580      590      600
      *      *      *      *      *
AGTTTTGAAA AGTCGTGGGT TAAAGTGAAA GATATTAAAA GCATTGGAGT
TCAAAACTTT TCAGCACCCA ATTTCACTTT CTATAATTTT CGTAACCTCA

      610      620      630      640      650
      *      *      *      *      *
AGATTTGATT ACGTGGACTC CAAGCAACGA CGTTGTATTG TTTCGTAGTA
TCTAAACTAA TGCACCTGAG GTTCGTTGCT GCAACATAAC AAAGCATCAT

      660      670      680      690      700
      *      *      *      *      *
GTGATCGTGG TTGCCTCTAC AACATAAACG CAGAGAAGTT GAATTTAGTT
CACTAGCACC AACGGAGATG TTGTATTTGC GTCTCTTCAA CTAAATCAA

      710      720      730      740      750
      *      *      *      *      *
TATGCAAAAA AAGAGGGATC TGATTGTTCT TTCGTTTGTT TTCCGTTTGTG
ATACGTTTTT TTCTCCCTAG ACTAACAAGA AAGCAAACAA AAGGCAAAAC

      760      770      780      790      800
      *      *      *      *      *
TTCTGATTAC GAGAGGGTTG ATCTGAACGG AAGAAGCAAC GGGCCGACAC
AAGACTAATG CTCTCCCAAC TAGACTTGCC TTCTTCGTTG CCCGGCTGTG

      810      820      830      840      850
      *      *      *      *      *
TTTAAAAAAA AAATAAAAAA AATGGGCCGA CAAATGCAAA CGTAGTTGAC
AAATTTTTTT TTTATTTTTT TTACCCGGCT GTTTACGTTT GCATCAACTG

      860      870      880      890      900
      *      *      *      *      *
AAGGATCTCA AGTCTCAAGT CTCAATTGGC TCGCTCATTG TGGGGCATAA
TTCCTAGAGT TCAGAGTTCA GAGTTAACCG AGCGAGTAAC ACCCCGTATT

      910      920      930      940      950
      *      *      *      *      *
ATATATCTAG TGATGTTTAA TTGTTTTTTA TAAGGTAAAA AGGAATATTG
TATATAGATC ACTACAAATT AACAAAAAAT ATTCCATTTT TCCTTATAAC

      960      970      980      990      1000
      *      *      *      *      *
AATTTTGTTT CTTAGGTTTA TGTAATAATA CCAAACATTG TTTTATGAAT
TTAAACAAA GAATCCAAAT ACATTATTAT GGTGTGTAAC AAAATACTTA

      1010      1020      1030      1040      1050
      *      *      *      *      *
ATTTAATCTG ATTTTTTGGC TAGTTATTTT ATTATATCAA GGGTTCCTGT
TAAATTAGAC TAAAAAACCG ATCAATAAAA TAATATAGTT CCCAAGGACA

      1060      1070      1080      1090      1100
      *      *      *      *      *

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08903334-030397

TTATAGTTGA	AAACAGTTAC	TGTATAGAAA	ATAGTGTCCC	AATTTTCTCT
AATATCAACT	TTTGTCAATG	ACATATCTTT	TATCACAGGG	TTAAAAAGAGA
1110	1120	1130	1140	1150
*	*	*	*	*
CTTAAATAAT	ATATTAGTTA	ATAAAAGATA	TTTTAATATA	TTAGATATAC
GAATTTATTA	TATAATCAAT	TATTTTCTAT	AAAATTATAT	AATCTATATG
1160	1170	1180	1190	1200
*	*	*	*	*
AATAATATCT	AAAGCAACAC	ATATTTAGAC	ACAACACGTA	ATATCTTACT
TTATTATAGA	TTTCGTTGTG	TATAAATCTG	TGTTGTGCAT	TATAGAATGA
1210	1220	1230	1240	1250
*	*	*	*	*
ATTGTTTACA	TATATTTATA	GCTTACCAAT	ATAACCCGTA	TCTATGTTTT
TAACAAATGT	ATATAAATAT	CGAATGGTTA	TATTGGGCAT	AGATACAAAA
1260	1270	1280	1290	1300
*	*	*	*	*
ATAAGCTTTT	ATACAATATA	TGTACGGTAT	GCTGTCCACG	TATATATATT
TATTCGAAAA	TATGTTATAT	ACATGCCATA	CGACAGGTGC	ATATATATAA
1310	1320	1330	1340	1350
*	*	*	*	*
CTCCAAAAAA	AACGCATGGT	ACACAAAATT	TATTAAATAT	TTGGCAATTG
GAGGTTTTTT	TTGCGTACCA	TGTGTTTTAA	ATAATTTATA	AACCGTTAAC
1360	1370	1380	1390	1400
*	*	*	*	*
GGTGTTTATC	TAAAGTTTAT	CACAATATTT	ATCAACTATA	ATAGATGGTA
CCACAAATAG	ATTTCAAATA	GTGTTATAAA	TAGTTGATAT	TATCTACCAT
1410	1420	1430	1440	1450
*	*	*	*	*
GAAGATAAAA	AAATTATATC	AGATTGATTC	AATTAAATTT	TATAATATAT
CTTCTATTTT	TTTAATATAG	TCTAACTAAG	TTAATTTAAA	ATATTATATA
1460	1470	1480	1490	1500
*	*	*	*	*
CATTTTAAAA	AATTAATTAA	AAGAAAACCTA	TTTCATAAAA	TTGTTCAAAA
GTAAAATTTT	TTAATTAATT	TTCTTTTGAT	AAAGTATTTT	AACAAGTTTT
1510	1520	1530	1540	1550
*	*	*	*	*
GATAATTAGT	AAAATTAATT	AAATATGTGA	TGCTATTGAA	TTATAGAGAG
CTATTAATCA	TTTTAATTAA	TTTATACACT	ACGATAACTT	AATATCTCTC
1560	1570	1580	1590	1600
*	*	*	*	*
TTATTGTAAA	TTTACTTAAA	ATCATACAAA	TCTTATCCTA	ATTTAACTTA
AATAACATTT	AAATGAATTT	TAGTATGTTT	AGAATAGGAT	TAAATTGAAT
1610	1620	1630	1640	1650

030334-00007

TCATTTAAGA	AATACAAAAG	TAAAAAACGC	GGAAAGCAAT	AATTTATTTA
AGTAAATTCT	TTATGTTTTC	ATTTTTTGCG	CCTTTCGTTA	TTAAATAAAAT
1660	1670	1680	1690	1700
CCTTATTATA	ACTCCTATAT	AAAGTACTCT	GTTTATTCAA	CATAATCTTA
GGAATAATAT	TGAGGATATA	TTTCATGAGA	CAAATAAGTT	GTATTAGAAT
1710	1720	1730	1740	1750
CGTTGTTGTA	TTTCATAGGCA	TCTTTAACCT	ATCTTTTCAT	TTTCTGATCT
GCAACAACAT	AAGTATCCGT	AGAAATTGGA	TAGAAAAGTA	AAAGACTAGA
1760	1770	1780	1790	1800
CGATCGTTTT	CGATCCAACA	AAATGAGTCT	ACCGGTGAGG	AACCAAGAGG
GCTAGCAAAA	GCTAGGTTGT	TTTACTCAGA	TGGCCACTCC	TTGGTTCTCC
1810	1820	1830	1840	1850
TGATTATGCA	GATTCCTTCT	TCTTCTCAGT	TTCCAGCAAC	ATCGAGTCCG
ACTAATACGT	CTAAGGAAGA	AGAAGAGTCA	AAGGTCGTTG	TAGCTCAGGC
1860	1870	1880	1890	1900
GAAAACACCA	ATCAAGTGAA	GGATGAGCCA	AATTTGTTTA	GACGTGTTAT
CTTTTGTGGT	TAGTTCACCT	CCTACTCGGT	TTAAACAAAT	CTGCACAATA
1910	1920	1930	1940	1950
GAATTTGCTT	TTACGTCGTA	GTTATTGAAA	AAGCTGATTT	ATCGCATGAT
CTTAAACGAA	AATGCAGCAT	CAATAACTTT	TTCGACTAAA	TAGCGTACTA
1960	1970	1980	1990	2000
TCAGAACGAG	AAGTTGAAGG	CAAATAACTA	AAGAAGTCTT	TTATATGTAT
AGTCTTGCTC	TTCAACTTCC	GTTTATTGAT	TTCTTCAGAA	AATATACATA
2010	2020	2030	2040	2050
ACAATAATTG	TTTTTAAATC	AAATCCTAAT	TAAAAAAATA	TATTCATTAT
TGTTATTAAC	AAAAATTAG	TTTAGGATTA	ATTTTTTTTAT	ATAAGTAATA
2060	2070	2080	2090	2100
GACTTTCATG	TTTTTAATGT	AATTTATTCC	TATATCTATA	ATGATTTTTG
CTGAAAGTAC	AAAAATTACA	TTAAATAAGG	ATATAGATAT	TACTAAAAAC
2110	2120	2130	2140	2150
TTGTGAAGAG	CGTTTTTCATT	TGCTATAGAA	CAAGGAGAAT	AGTTCAGGA
AACACTTCTC	GCAAAAGTAA	ACGATATCTT	GTTCTCTCTA	TCAAGGTCCT

03030304-030303

2160	2170	2180	2190	2200
*	*	*	*	*
AATATTCGAC	TTGATTTAAT	TATAGTGTA	ACATGCTGAA	CACTGAAAAT
TTATAAGCTG	AACTAAATTA	ATATCACATT	TGTACGACTT	GTGACTTTTA
2210	2220	2230	2240	2250
*	*	*	*	*
TACTTTTTCA	ATAAACGAAA	AATATAATAT	ACATTACAAA	ACTTATGTGA
ATGAAAAAGT	TATTTGCTTT	TTATATTATA	TGTAATGTTT	TGAATACACT
2260	2270	2280	2290	2300
*	*	*	*	*
ATAAAGCATG	AGACTTAATA	TACGTTCCCT	TTATCATTTT	ACTTCAAAGA
TATTTTCGTAC	TCTGAATTAT	ATGCAAGGGA	AATAGTAAAA	TGAAGTTTCT
2310	2320	2330	2340	2350
*	*	*	*	*
AAATAAACAG	AAATGTAAC	TTCACATGTA	AATCTAATTC	TTAAATTTAA
TTTATTTGTC	TTTACATTGA	AAGTGATCAT	TTAGATTAA	AATTTAAATT
2360	2370	2380	2390	2400
*	*	*	*	*
AAAATAATAT	TTATATATTT	ATATGAAAAT	AACGAACCGG	ATGAAAAATA
TTTTATTATA	AATATATAAA	TATACTTTTA	TTGCTTGGCC	TACTTTTTAT
2410	2420	2430	2440	2450
*	*	*	*	*
AATTTTATAT	ATTTATATCA	TCTCCAAATC	TAGTTTGGTT	CAGGGGCTTA
TTAAATATA	TAAATATAGT	AGAGGTTTAG	ATCAAACCAA	GTCCCCGAAT
2460	2470	2480	2490	2500
*	*	*	*	*
CCGAACCGGA	TTGAACTTCT	CATATACAAA	AATTAGCAAC	ACAAAATGTC
GGCTTGGCCT	AACTTGAAGA	GTATATGTTT	TTAATCGTTG	TGTTTTACAG
2510	2520	2530	2540	2550
*	*	*	*	*
TCCGGTATAA	ATACTAACAT	TTATAACCCG	AACCGGTTTA	GCTTCCTGTT
AGGCCATATT	TATGATTGTA	AATATTGGGC	TTGGCCAAAT	CGAAGGACAA
2560	2570	2580	2590	2600
*	*	*	*	*
ATATCTTTTT	AAAAAAGATC	TCTGACAAAG	ATTCCTTTCC	TGGAAATTTA
TATAGAAAAA	TTTTTTCTAG	AGACTGTTTC	TAAGGAAAGG	ACCTTTAAAT
2610	2620	2630	2640	2650
*	*	*	*	*
CCGGTTTTGG	TGAAATGTAA	ACCGTGGGAC	GAGGATGCTT	CTTCATATCT
GGCCAAAACC	ACTTTACATT	TGGCACCTTG	CTCCTACGAA	GAAGTATAGA
2660	2670	2680	2690	2700
*	*	*	*	*
CACCACCACT	CTCGTTGACT	GGACTTGGCT	CTGCTCGTCA	ATGGTTATCT
GTGGTGGTGA	GAGCAACTGA	CCTGAACCGA	GACGAGCAGT	TACCAATAGA

269097 1280550



2710	2720	2730	2740	2750
*	*	*	*	*
TCGATCTTAA	ACCAAATCCA	GTTGATAAGG	TCTCTTCGTT	GATTAGCAGA
AGCTAGAATT	TGGTTTAGGT	CAACTATTCC	AGAGAAGCAA	CTAATCGTCT
2760	2770	2780	2790	2800
*	*	*	*	*
GATCTCTTTA	ATTTGTGAAT	TTCAATTCAT	CGGAACCTGT	TGATGGACAC
CTAGAGAAAT	TAAACACTTA	AAGTTAAGTA	GCCTTGGACA	ACTACCTGTG
2810	2820	2830	2840	2850
*	*	*	*	*
CACCATTGAT	GGATTCGCCG	ATTCTTATGA	AATCAGCAGC	ACTAGTTTCG
GTGGTAACTA	CCTAAGCGGC	TAAGAATACT	TTAGTCGTCG	TGATCAAAGC
2860	2870	2880	2890	2900
*	*	*	*	*
TCGCTACCGA	TAACACCGAC	TCCTCTATTG	TTTATCTGGC	CGCCGAACAA
AGCGATGGCT	ATTGTGGCTG	AGGAGATAAC	AAATAGACCG	GCGGCTTGTT
2910	2920	2930	2940	2950
*	*	*	*	*
GTA CTACCG	GACCTGATGT	ATCTGCTCTG	CAATTGCTCT	CCAACAGCTT
CATGAGTGGC	CTGGACTACA	TAGACGAGAC	GTTAACGAGA	GGTTGTCGAA
2960	2970	2980	2990	3000
*	*	*	*	*
CGAATCCGTC	TTTGACTCGC	CGGATGATTT	CTACAGCGAC	GCTAAGCTTG
GCTTAGGCAG	AACTGAGCG	GCCTACTAAA	GATGTCGCTG	CGATTCGAAC
3010	3020	3030	3040	3050
*	*	*	*	*
TTCTCTCCGA	CGGCCGGGAA	GTTTCTTTCC	ACCGGTGCGT	TTTGTCAGCG
AAGAGAGGCT	GCCGGCCCTT	CAAAGAAAGG	TGGCCACGCA	AAACAGTCGC
3060	3070	3080	3090	3100
*	*	*	*	*
AGAAGCTCTT	TCTTCAAGAG	CGCTTTAGCC	GCCGCTAAGA	AGGAGAAAGA
TCTTCGAGAA	AGAAGTTCTC	GCGAAATCGG	CGGCGATTCT	TCCTCTTTCT
3110	3120	3130	3140	3150
*	*	*	*	*
CTCCAACAAC	ACCGCCGCCG	TGAAGCTCGA	GCTTAAGGAG	ATTGCCAAGG
GAGGTTGTTG	TGGCGGCGGC	ACTTCGAGCT	CGAATTCCTC	TAACGGTTCC
3160	3170	3180	3190	3200
*	*	*	*	*
ATTACGAAGT	CGGTTTCGAT	TCGGTTGTGA	CTGTTTTGGC	TTATGTTTAC
TAATGCTTCA	GCCAAAGCTA	AGCCAACACT	GACAAAACCG	AATACAAATG
3210	3220	3230	3240	3250
*	*	*	*	*
AGCAGCAGAG	TGAGACCGCC	GCCTAAAGGA	GTTTCTGAAT	GCGCAGACGA

CGCGCTTGTT

TCGTCGTCTC	ACTCTGGCGG	CGGATTTCCT	CAAAGACTTA	CGCGTCTGCT
3260	3270	3280	3290	3300
*	*	*	*	*
GAATTGCTGC	CACGTGGCTT	GCCGGCCGGC	GGTGGATTTT	ATGTTGGAGG
CTTAACGACG	GTGCACCGAA	CGGCCGGCCG	CCACCTAAAG	TACAACCTCC
3310	3320	3330	3340	3350
*	*	*	*	*
TTCTCTATTT	GGCTTTCATC	TTCAAGATCC	CTGAATTAAT	TACTCTCTAT
AAGAGATAAA	CCGAAAGTAG	AAGTTCTAGG	GACTTAATTA	ATGAGAGATA
3360	3370	3380	3390	3400
*	*	*	*	*
CAGGTAAAAC	ACCATCTGCA	TTAAGCTATG	GTTACACATT	CATGAATATG
GTCCATTTTG	TGGTAGACGT	AATTCGATAC	CAATGTGTAA	GTACTTATAC
3410	3420	3430	3440	3450
*	*	*	*	*
TTCTTACTTG	AGTACTTGTA	TTTGTATTTT	AGAGGCACTT	ATTGGACGTT
AAGAATGAAC	TCATGAACAT	AAACATAAAG	TCTCCGTGAA	TAACCTGCAA
3460	3470	3480	3490	3500
*	*	*	*	*
GTAGACAAAG	TTGTTATAGA	GGACACATTG	GTTATACTCA	AGCTTGCTAA
CATCTGTTTC	AACAATATCT	CCTGTGTAAC	CAATATGAGT	TCGAACGATT
3510	3520	3530	3540	3550
*	*	*	*	*
TATATGTGGT	AAAGCTTGTA	TGAAGCTATT	GGATAGATGT	AAAGAGATTA
ATATACACCA	TTTCGAACAT	ACTTCGATAA	CCTATCTACA	TTTCTCTAAT
3560	3570	3580	3590	3600
*	*	*	*	*
TTGTCAAGTC	TAATGTAGAT	ATGGTTAGTC	TTGAAAAGTC	ATTGCCGGAA
AACAGTTCAG	ATTACATCTA	TACCAATCAG	AACTTTTCAG	TAACGGCCTT
3610	3620	3630	3640	3650
*	*	*	*	*
GAGCTTGTTA	AAGAGATAAT	TGATAGACGT	AAAGAGCTTG	GTTTGGAGGT
CTCGAACAAT	TTCTCTATTA	ACTATCTGCA	TTTCTCGAAC	CAAACCTCCA
3660	3670	3680	3690	3700
*	*	*	*	*
ACCTAAAGTA	AAGAAACATG	TCTCGAATGT	ACATAAGGCA	CTTGACTCGG
TGGATTTTCAT	TTCTTTGTAC	AGAGCTTACA	TGTATTCCGT	GAAC TGAGCC
3710	3720	3730	3740	3750
*	*	*	*	*
ATGATATTGA	GTTAGTCAAG	TTGCTTTTGA	AAGAGGATCA	CACCAATCTA
TACTATAACT	CAATCAGTTC	AACGAAAAC	TTCTCCTAGT	GTGGTTAGAT
3760	3770	3780	3790	3800
*	*	*	*	*

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GATGATGCGT	GTGCTCTTCA	TTTCGCTGTT	GCATATTGCA	ATGTGAAGAC
CTACTACGCA	CACGAGAAGT	AAAGCGACAA	CGTATAACGT	TACACTTCTG
3810	3820	3830	3840	3850
*	*	*	*	*
CGCAACAGAT	CTTTTAAAC	TTGATCTTGC	CGATGTCAAC	CATAGGAATC
GCGTTGTCTA	GAAAATTTTG	AACTAGAACG	GCTACAGTTG	GTATCCTTAG
3860	3870	3880	3890	3900
*	*	*	*	*
CGAGGGGATA	TACGGTGCTT	CATGTTGCTG	CGATGCGGAA	GGAGCCACAA
GCTCCCCTAT	ATGCCACGAA	GTACAACGAC	GCTACGCCTT	CCTCGGTGTT
3910	3920	3930	3940	3950
*	*	*	*	*
TTGATACTAT	CTCTATTGGA	AAAAGGTGCA	AGTGCATCAG	AAGCAACTTT
AACTATGATA	GAGATAACCT	TTTCCACGT	TCACGTAGTC	TTTCGTTGAA
3960	3970	3980	3990	4000
*	*	*	*	*
GGAAGGTAGA	ACCGCACTCA	TGATCGCAAA	ACAAGCCACT	ATGGCGGTTG
CCTTCCATCT	TGGCGTGAGT	ACTAGCGTTT	TGTTCCGGTGA	TACCGCCAAC
4010	4020	4030	4040	4050
*	*	*	*	*
AATGTAATAA	TATCCCGGAG	CAATGCAAGC	ATTCTCTCAA	AGGCCGACTA
TTACATTATT	ATAGGGCCTC	GTTACGTTTCG	TAAGAGAGTT	TCCGGCTGAT
4060	4070	4080	4090	4100
*	*	*	*	*
TGTGTAGAAA	TACTAGAGCA	AGAAGACAAA	CGAGAACAAA	TTCCTAGAGA
ACACATCTTT	ATGATCTCGT	TCTTCTGTTT	GCTCTTGTTT	AAGGATCTCT
4110	4120	4130	4140	4150
*	*	*	*	*
TGTTCTCTCC	TCTTTTGCGAG	TGGCGGCCGA	TGAATTGAAG	ATGACGCTGC
ACAAGGAGGG	AGAAAACGTC	ACCGCCGGCT	ACTTAACTTC	TACTGCGACG
4160	4170	4180	4190	4200
*	*	*	*	*
TCGATCTTGA	AAATAGAGGT	ATCTATCAAG	TCTTATTTCT	TATATGTTTG
AGCTAGAACT	TTTATCTCCA	TAGATAGTTC	AGAATAAAGA	ATATACAAAC
4210	4220	4230	4240	4250
*	*	*	*	*
AATTAAATTT	ATGTCCTCTC	TATTAGGAAA	CTGAGTGAAC	TAATGATAAC
TTAATTTAAA	TACAGGAGAG	ATAATCCTTT	GACTCACTTG	ATTACTATTG
4260	4270	4280	4290	4300
*	*	*	*	*
TATTCTTTGT	GTCGTCCACT	GTTTAGTTGC	ACTTGCTCAA	CGTCTTTTTC
ATAAGAAACA	CAGCAGGTGA	CAAATCAACG	TGAACGAGTT	GCAGAAAAAG
4310	4320	4330	4340	4350

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	*		*		*		*		*
CAACGGAAGC	ACAAGCTGCA	ATGGAGATCG	CCGAAATGAA	GGGAACATGT					
GTTGCCTTCG	TGTTTCGACGT	TACCTCTAGC	GGCTTTACTT	CCCTTGTA					
4360	4370	4380	4390	4400					
*	*	*	*	*					
GAGTTCATAG	TGACTAGCCT	CGAGCCTGAC	CGTCTCACTG	GTACGAAGAG					
CTCAAGTATC	ACTGATCGGA	GCTCGGACTG	GCAGAGTGAC	CATGCTTCTC					
4410	4420	4430	4440	4450					
*	*	*	*	*					
AACATCACCG	GGTGTAAAGA	TAGCACCTTT	CAGAATCCTA	GAAGAGCATC					
TTGTAGTGGC	CCACATTTCT	ATCGTGGA	GTCTTAGGAT	CTTCTCGTAG					
4460	4470	4480	4490	4500					
*	*	*	*	*					
AAAGTAGACT	AAAAGCGCTT	TCTAAAACCG	GTATGGATTC	TCACCCACTT					
TTTCATCTGA	TTTTTCGCGAA	AGATTTTG	CATACCTAAG	AGTGGGTGAA					
4510	4520	4530	4540	4550					
*	*	*	*	*					
CATCGGACTC	CTTATCACAA	AAAACAAAAC	TAAATGATCT	TTAAACATGG					
GTAGCCTGAG	GAATAGTGTT	TTTTGTTTTG	ATTTACTAGA	AATTTGTACC					
4560	4570	4580	4590	4600					
*	*	*	*	*					
TTTTGTTACT	TGCTGTCTGA	CCTTGTTTTT	TTATCATCAG	TGGAACTCGG					
AAAAACAATGA	ACGACAGACT	GGAACAAAAA	AATAGTAGTC	ACCTTGAGCC					
4610	4620	4630	4640	4650					
*	*	*	*	*					
GAAACGATTC	TTCCCGCGCT	GTTCGGCAGT	GCTCGACCAG	ATTATGA <td></td> <td></td> <td></td> <td></td> <td></td>					
CTTTGCTAAG	AAGGGCGCGA	CAAGCCGTCA	CGAGCTGGTC	TAATACTTGA					
4660	4670	4680	4690	4700					
*	*	*	*	*					
GTGAGGACTT	GA <td>GCTTGCGGAG</td> <td>AAGACGACAC</td> <td>TGCTGAAGAA</td> <td></td> <td></td> <td></td> <td></td> <td></td>	GCTTGCGGAG	AAGACGACAC	TGCTGAAGAA					
C <td>CTGAGTTGAC</td> <td>CGAACGCCTC</td> <td>TTCTGCTGTG</td> <td>ACGACTTCTT</td> <td></td> <td></td> <td></td> <td></td> <td></td>	CTGAGTTGAC	CGAACGCCTC	TTCTGCTGTG	ACGACTTCTT					
4710	4720	4730	4740	4750					
*	*	*	*	*					
ACGACTACAA	AAGAAGCAAA	GGTACATGGA	AATACAAGAG	ACACTAAAGA					
TGCTGATGTT	TTCTTCGTTT	CCATGTACCT	TTATGTTCTC	TGTGATTTCT					
4760	4770	4780	4790	4800					
*	*	*	*	*					
AGGCCTTTAG	TGAGGACAAT	TTGGAATTAG	GAAATTCGTC	CCTGACAGAT					
TCCGGAATC	ACTCCTGTTA	AACCTTAATC	CTTTAAGCAG	GGACTGTCTA					
4810	4820	4830	4840	4850					
*	*	*	*	*					
TCGACTTCTT	CCACATCGAA	ATCAACCGGT	GGAAAGAGGT	CTAACCGTAA					
AGCTGAAGAA	GGTGTAGCTT	TAGTTGGCCA	CCTTTCTCCA	GATTGGCATC					

4860	4870	4880	4890	4900
*	*	*	*	*
ACTCTCTCAT	CGTCGTCGGT	GAGACTCTTG	CCTCTTAGTG	TAATTTTTGC
TGAGAGAGTA	GCAGCAGCCA	CTCTGAGAAC	GGAGAATCAC	ATTAAAAACG
4910	4920	4930	4940	4950
*	*	*	*	*
TGTACCATAT	AATTCTGTTT	TCATGATGAC	TGTAAGTGT	TATGTCTATC
ACATGGTATA	TTAAGACAAA	AGTACTACTG	ACATTGACAA	ATACAGATAG
4960	4970	4980	4990	5000
*	*	*	*	*
GTTGGCGTCA	TATAGTTTCG	CTCTTCGTTT	TGCATCCTGT	GTATTATTGC
CAACCGCAGT	ATATCAAAGC	GAGAAGCAAA	ACGTAGGACA	CATAATAACG
5010	5020	5030	5040	5050
*	*	*	*	*
TGCAGGTGTG	CTTCAAACAA	ATGTTGTAAC	AATTTGAACC	AATGGTATAC
ACGTCCACAC	GAAGTTTGTT	TACAACATTG	TTAAACTTGG	TTACCATATG
5060	5070	5080	5090	5100
*	*	*	*	*
AGATTTGTAA	TATATATTTA	TGTACATCAA	CAATAACCCA	TGATGGTGT
TCTAAACATT	ATATATAAAT	ACATGTAGTT	GTTATTGGGT	ACTACCACAA
5110	5120	5130	5140	5150
*	*	*	*	*
ACAGAGTTGC	TAGAATCAAA	GTGTGAAATA	ATGTCAAATT	GTTTCATCTGT
TGTCTCAACG	ATCTTAGTTT	CACACTTTAT	TACAGTTTAA	CAAGTAGACA
5160	5170	5180	5190	5200
*	*	*	*	*
TGGATATTTT	CCACCAAGAA	CCAAAAGAAT	ATTCAAGTTC	CCTGAAGTTC
ACCTATAAAA	GGTGGTTCTT	GGTTTTCTTA	TAAGTTCAAG	GGACTTGAAG
5210	5220	5230	5240	5250
*	*	*	*	*
TGGCAACATT	CATGTTATAT	GTATCTTCCT	AATTCTTCCT	TTAACCTTTT
ACCGTTGTAA	GTACAATATA	CATAGAAGGA	TTAAGAAGGA	AATTGGAAAA
5260	5270	5280	5290	5300
*	*	*	*	*
GTAAGTCGAA	TTACACAGCA	AGTTAGTTTC	AGGTCTAGAG	ATAAGAGAAC
CATTGAGCTT	AATGTGTCGT	TCAATCAAAG	TCCAGATCTC	TATTCTCTTG
5310	5320	5330	5340	5350
*	*	*	*	*
ACTGAGTGGG	CGTGTAAGGT	GCATTCTCCT	AGTCAGCTCC	ATTGCATCCA
TGACTCACCC	GCACATTCCA	CGTAAGAGGA	TCAGTCGAGG	TAACGTAGGT
5360	5370	5380	5390	5400
*	*	*	*	*
ACATTTGTGA	ATGACACAAG	TTAACAATCC	TTTGCAACAT	TTCTGGGTGC
TGTAAACACT	TACTGTGTTC	AATTGTTAGG	AAACGTGGTA	AAGACCCACG

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Figure 1. The effect of the concentration of the *Agaricus bisporus* spores on the growth of *Agaricus bisporus* on the substrate. The concentration of the spores was 10<sup>4</sup> (a), 10<sup>5</sup> (b), 10<sup>6</sup> (c), 10<sup>7</sup> (d), 10<sup>8</sup> (e) and 10<sup>9</sup> (f) spores/g substrate. The substrate was a mixture of 100 g of wheat bran and 100 g of rice bran. The substrate was incubated at 25 °C for 7 days. The diameter of the mycelium was measured at the end of the incubation period. The diameter of the mycelium was 1.5 cm (a), 1.8 cm (b), 2.1 cm (c), 2.4 cm (d), 2.7 cm (e) and 3.0 cm (f).

FIG. 4

Sheet 12 of 14

7010	7020	7030	7040	7050
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1. **Introduction**  
 2. **Background**  
 3. **Methodology**  
 4. **Results**  
 5. **Discussion**  
 6. **Conclusion**  
 7. **References**  
 8. **Appendix**  
 9. **Figure 1**  
 10. **Figure 2**  
 11. **Figure 3**  
 12. **Figure 4**  
 13. **Figure 5**  
 14. **Figure 6**  
 15. **Figure 7**  
 16. **Figure 8**  
 17. **Figure 9**  
 18. **Figure 10**  
 19. **Figure 11**  
 20. **Figure 12**  
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 217. **Figure 209**



	*		*		*		*		*
AGGATGATAA	CTTGGAAGCTT	CAAGCATAGT	CTCCAAACTA	GTGTCGTTCA					
TCCTACTATT	GAACCTTGAA	GTTTCGTATCA	GAGGTTTGAT	CACAGCAAGT					
7060	7070	7080	7090	7100					
*	*	*	*	*					
CTACATGAAG	AAGTAGATAG	ATAAAGAGAT	CCGGTGAAAC	AACTACAGGA					
GATGTACTTC	TTCATCTATC	TATTTCTCTA	GGCCACTTTG	TTGATGTCCT					
7110	7120	7130	7140	7150					
*	*	*	*	*					
TACTTACCAA	AATATATTGA	ACACTGATTT	CTGCAGCTGC	AATCCAAAAA					
ATGAATGGTT	TTATATAACT	TGTGACTAAA	GACGTCGACG	TTAGGTTTTT					
7160	7170	7180	7190	7200					
*	*	*	*	*					
TTGGATAAAG	ACCATTCAAC	AATGTACTTA	ACGCAGTCTT	TTGCCTAACC					
AACCTATTTC	TGGTAAGTTG	TTACATGAAT	TGCGTCAGAA	AACGGATTGG					
7210	7220	7230	7240	7250					
*	*	*	*	*					
TTGACCGTTT	TAGGAGTGGA	TCCTTCATAG	TAAACACCAT	CAGGACCATA					
AACTGGCAAA	ATCCTCACCT	AGGAAGTATC	ATTTGTGGTA	GTCCTGGTAT					
7260	7270	7280	7290	7300					
*	*	*	*	*					
CTTGGTAGAA	CCTTTCTCTC	AAGGTTTCCA	TCGCCATGAC	CATAACAGTC					
GAACCATCTT	GGAAAGAGAG	TTCCAAAGGT	AGCGGTACTG	GTATTGTCAG					
7310	7320	7330	7340	7350					
*	*	*	*	*					
CTGCAGTGAA	TTCTAAGAAA	AATGTAAAAA	ATTTTGGCCT	AAACTCATAA					
GACGTCACCT	AAGATTCTTT	TTACATTTTT	TAAACCGGA	TTTGAGTATT					
7360	7370	7380	7390	7400					
*	*	*	*	*					
TTCTTAACAT	ACGAAACCAT	GGAGAACTCC	ATGTCTAAAA	AATAAAGGCT					
AAGAATTGTA	TGCTTTGGTA	CCTCTTGAGG	TACAGATTTT	TTATTTCCGA					
7410	7420	7430	7440	7450					
*	*	*	*	*					
AAAGCTTTTT	GGCGACAGAA	GCAGATAAAT	CCATTCAAAA	CACATAAACT					
TTTCGAAAAA	CCGCTGTCTT	CGTCTATTTA	GGTAAGTTTT	GTGTATTTGA					
7460	7470	7480	7490	7500					
*	*	*	*	*					
CTAAACAATA	AACAGTGATA	CTCAATACTA	AGACTTGTA	AGGTCTACGT					
GATTTGTTAT	TTGTCACAT	GAGTTATGAT	TCTGAACATT	TCCAGATGCA					
7510	7520	7530	7540						
*	*	*	*						
AACTCAAAAC	TGGAGAATTG	TCAGATCGGG	TGTGGCTAGT	AGAAGCTT					
TTGAGTTTTG	ACCTCTTAAC	AGTCTAGCCC	ACACCGATCA	TCTTCGAA					

10	20	30	40	50
*	*	*	*	*
TCGATCTTTA	ACCAAATCCA	GTTGATAAGG	TCTCTTCGTT	GATTAGCAGA
AGCTAGAAAT	TGGTTTAGGT	CAACTATTCC	AGAGAAGCAA	CTAATCGTCT
60	70	80	90	100
*	*	*	*	*
GATCTCTTTA	ATTTGTGAAT	TTCAATTCAT	CGGAACCTGT	TGATGGACAC
CTAGAGAAAT	TAAACACTTA	AAGTTAAGTA	GCCTTGGACA	ACTACCTGTG
				M D T>
110	120	130	140	150
*	*	*	*	*
CACCATTGAT	GGATTTCGCCG	ATTCTTATGA	AATCAGCAGC	ACTAGTTTTCG
GTGGTAACTA	CCTAAGCGGC	TAAGAATACT	TTAGTCGTCG	TGATCAAAGC
T I D	G F A	D S Y E	I S S	T S F>
160	170	180	190	200
*	*	*	*	*
TCGCTACCGA	TAACACCGAC	TCCTCTATTG	TTTATCTGGC	CGCCGAACAA
AGCGATGGCT	ATTGTGGCTG	AGGAGATAAC	AAATAGACCG	GCGGCTTGTT
V A T D	N T D	S S I	V Y L A	A E Q>
210	220	230	240	250
*	*	*	*	*
GTACTCACCG	GACCTGATGT	ATCTGCTCTG	CAATTGCTCT	CCAACAGCTT
CATGAGTGGC	CTGGACTACA	TAGACGAGAC	GTTAACGAGA	GGTTGTGCGAA
V L T	G P D V	S A L	Q L L	S N S F>
260	270	280	290	300
*	*	*	*	*
CGAATCCGTC	TTTGACTCGC	CGGATGATTT	CTACAGCGAC	GCTAAGCTTG
GCTTAGGCAG	AAACTGAGCG	GCCTACTAAA	GATGTCGCTG	CGATTCTGAAC
E S V	F D S	P D D F	Y S D	A K L>
310	320	330	340	350
*	*	*	*	*
TTCTCTCCGA	CGGCCGGGAA	GTTTCTTTTC	ACCGGTGCGT	TTTGTCTAGCG
AAGAGAGGCT	GCCGGCCCTT	CAAAGAAAGG	TGGCCACGCA	AAACAGTCGC
V L S D	G R E	V S F	H R C V	L S A>
360	370	380	390	400
*	*	*	*	*
AGAAGCTCTT	TCTTCAAGAG	CGCTTTAGCC	GCCGCTAAGA	AGGAGAAAGA
TCTTCGAGAA	AGAAGTTCTC	GCGAAATCGG	CGGCGATTCT	TCCTCTTTCT
R S S	F F K S	A L A	A A K	K E K D>
410	420	430	440	450
*	*	*	*	*
CTCCAACAAC	ACCGCCGCCG	TGAAGCTCGA	GCTTAAGGAG	ATTGCCAAGG
GAGGTTGTTG	TGGCGGCGGC	ACTTCGAGCT	CGAATTCCTC	TAACGGTTCC
S N N	T A A	V K L E	L K E	I A K>

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      460      470      480      490      500
      *        *        *        *        *
ATTACGAAGT CGGTTTCGAT TCGGTTGTGA CTGTTTTGGC TTATGTTTAC
TAATGCTTCA GCCAAAGCTA AGCCAACACT GACAAAACCG AATACAAATG
D Y E V   G F D   S V V   T V L A   Y V Y>

      510      520      530      540      550
      *        *        *        *        *
AGCAGCAGAG TGAGACCGCC GCCTAAAGGA GTTTCTGAAT GCGCAGACGA
TCGTCGTCTC ACTCTGGCGG CGGATTTCTT CAAAGACTTA CGCGTCTGCT
S S R   V R P P   P K G   V S E   C A D E>

      560      570      580      590      600
      *        *        *        *        *
GAATTGCTGC CACGTGGCTT GCCGGCCGGC GGTGGATTTC ATGTTGGAGG
CTTAACGACG GTGCACCGAA CGGCCGGCCG CCACCTAAAG TACAACCTCC
N C C   H V A   C R P A   V D F   M L E>

      610      620      630      640      650
      *        *        *        *        *
TTCTCTATTT GGCTTTCATC TTCAAGATCC CTGAATTAAT TACTCTCTAT
AAGAGATAAA CCGAAAGTAG AAGTTCTAGG GACTTAATTA ATGAGAGATA
V L Y L   A F I   F K I   P E L I   T L Y>

      660      670      680      690      700
      *        *        *        *        *
CAGAGGCACT TATTGGACGT TGTAGACAAA GTTGTTATAG AGGACACATT
GTCTCCGTGA ATAACCTGCA ACATCTGTTT CAACAATATC TCCTGTGTAA
Q R H   L L D V   V D K   V V I   E D T L>

      710      720      730      740      750
      *        *        *        *        *
GGTTATACTC AAGCTTGCTA ATATATGTGG TAAAGCTTGT ATGAAGCTAT
CCAATATGAG TTCGAACGAT TATATACACC ATTTCTGAACA TACTTCGATA
V I L   K L A   N I C G   K A C   M K L>

      760      770      780      790      800
      *        *        *        *        *
TGGATAGATG TAAAGAGATT ATTGTCAAGT CTAATGTAGA TATGGTTAGT
ACCTATCTAC ATTTCTCTAA TAACAGTTCA GATTACATCT ATACCAATCA
L D R C   K E I   I V K   S N V D   M V S>

      810      820      830      840      850
      *        *        *        *        *
CTTGAAAAGT CATTGCCGGA AGAGCTTGTT AAAGAGATAA TTGATAGACG
GAACTTTTCA GTAACGGCCT TCTCGAACAA TTTCTCTATT AACTATCTGC
L E K   S L P E   E L V   K E I   I D R R>

      860      870      880      890      900
      *        *        *        *        *
TAAAGAGCTT GGTTTGGAGG TACCTAAAGT AAAGAAACAT GTCTCGAATG
ATTTCTCGAA CCAAACCTCC ATGGATTTC TTTCTTTGTA CAGAGCTTAC
K E L   G L E   V P K V   K K H   V S N>

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          910          920          930          940          950
          *           *           *           *           *
TACATAAGGC ACTTGACTCG GATGATATTG AGTTAGTCAA GTTGCTTTTG
ATGTATTCCG TGAAGTGAAG CTACTATAAC TCAATCAGTT CAACGAAAAC
V H K A   L D S   D D I   E L V K   L L L>

          960          970          980          990          1000
          *           *           *           *           *
AAAGAGGATC ACACCAATCT AGATGATGCG TGTGCTCTTC ATTTTCGCTGT
TTTCTCCTAG TGTGGTTAGA TCTACTACGC ACACGAGAAG TAAAGCGACA
K E D   H T N L   D D A   C A L   H F A V>

          1010         1020         1030         1040         1050
          *           *           *           *           *
TGCATATTGC AATGTGAAGA CCGCAACAGA TCTTTTAAAA CTTGATCTTG
ACGTATAACG TTACACTTCT GGC GTTGTCT AGAAAATTTT GAACTAGAAC
A Y C   N V K   T A T D   L L K   L D L>

          1060         1070         1080         1090         1100
          *           *           *           *           *
CCGATGTCAA CCATAGGAAT CCGAGGGGAT ATACGGTGCT TCATGTTGCT
GGCTACAGTT GGTATCCTTA GGCTCCCCTA TATGCCACGA AGTACAACGA
A D V N   H R N   P R G   Y T V L   H V A>

          1110         1120         1130         1140         1150
          *           *           *           *           *
GCGATGCGGA AGGAGCCACA ATTGATACTA TCTCTATTGG AAAAAGGTGC
CGCTACGCCCT TCCTCGGTGT TAACTATGAT AGAGATAACC TTTTTCACGC
A M R   K E P Q   L I L   S L L   E K G A>

          1160         1170         1180         1190         1200
          *           *           *           *           *
AAGTGCATCA GAAGCAACTT TGGAAGGTAG AACCGCACTC ATGATCGCAA
TTCACGTAGT CTTTCGTTGAA ACCTTCCATC TTGGCGTGAG TACTAGCGTT
S A S   E A T   L E G R   T A L   M I A>

          1210         1220         1230         1240         1250
          *           *           *           *           *
AACAAAGCCAC TATGGCGGTT GAATGTAATA ATATCCCGGA GCAATGCAAG
TTGTTTCGGTG ATACCGCCAA CTTACATTAT TATAGGGCCT CGTTACGTTT
K Q A T   M A V   E C N   N I P E   Q C K>

          1260         1270         1280         1290         1300
          *           *           *           *           *
CATTCTCTCA AAGGCCGACT ATGTGTAGAA ATACTAGAGC AAGAAGACAA
GTAAGAGAGT TTCCGGCTGA TACACATCTT TATGATCTCG TTCTTCTGTT
H S L   K G R L   C V E   I L E   Q E D K>

          1310         1320         1330         1340         1350
          *           *           *           *           *
ACGAGAACAA ATTCCCTAGAG ATGTTCCCTC CTCTTTTGCA GTGGCGGCCG
TGCTCTTGTT TAAGGATCTC TACAAGGAGG GAGAAAACGT CACCGCCGGC
R E Q   I P R   D V P P   S F A   V A A>

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2690334-1330580

[illegible]

AAAA  
TTTT

[illegible]

FIG. 6A

NPR1 (323) NHRNPRGYTVLHVAAAMRKEPQLILSLLEKGAASEATLEGR TALMI AKQ (371)  
 N + GYT LH AA + +I LL+ AS +E T+ G TAL IA++  
 ankyrin 3 (740) NAKTKNGYTALHQAAQQGHTHIINVLLQNNASPNELTVNGNTALAIARR (788)

NPR1 (262) KVKKHVSNNVHKALDSDDI ELVKLLKED (289)  
 K K +S +H A D + V+LLL+ +  
 ankyrin 3 (313) KTKNGLSPLHMA TQGDHLNCVQLLSRN (340)

FIG. 6B

1st repeat (265) KHVSNNVHKALDSDDI ELVKLLKEDHTNLDDAC (297)  
 2nd repeat (294) DDACALHFVAVAYCNVKTATD LKLDLADVNHRN (326)  
 3rd repeat (328) RGYTVLHVAAAMRKEPQLILSLLEKGAASEATL (360)  
 4th repeat (361) EGRTALMI AKQATMAVECN NIPEQCKHSLKGRL (393)

ANK consensus  
 (Michaely and Bennett) G TPLHLAAR GHVEVVKKLLLD GADVNA TK  
 A I SQ NNLDIAEV K NPD D  
 V K T M R Q SI N  
 E

(Bork) t otLHhah tt thht LLt t t

10	20	30	40	50
*	*	*	*	*
GTGACTTTCT	AACATATGGCT	GAAATTGCAG	AACGAAAAAG	ACTTTCCATT
CACTGAAAGA	TTGATACCGA	CTTTAACGTC	TTGCTTTTTC	TGAAAGGTAA
60	70	80	90	100
*	*	*	*	*
TTTCACTTGA	ATGAAACCCA	AAATGGGAAAT	CTATCTCTCT	TCTTCTTCTC
AAAGTGAAC	TACTTTGGGT	TTTACCTTTA	GATAGAGAGA	AGAAGAAGAG
110	120	130	140	150
*	*	*	*	*
TTTTACTACC	TCCATTTC	TGGCTTTCCC	TCCTCTACCT	TCCCTAGCTC
AAAATGATGG	AGGTAAAGGT	ACCGAAAGGG	AGGAGATGGA	AGGGATCGAG
160	170	180	190	200
*	*	*	*	*
TTTTCAATTT	CTAGAATATT	CTTTTCTTAG	TCTGTAATTA	TCTATAGCTC
AAAAGTTAAA	GATCTTATAA	GAAAAAGAATC	AGACATTAAT	AGATATCGAG
210	220	230	240	250
*	*	*	*	*
AATTTCTAAG	ACAGAACTTA	TGTAAGGCGG	CTTTCTGTAA	TGGATAATAG
TTAAAGATTC	TGTCTTGAAT	ACATTCCGCC	GAAAGACATT	ACCTATTATC
260	270	280	290	300
*	*	*	*	*
TAGGACTGCG	TTTTCTGATT	CGAATGACAT	CAGCGGAAGC	AGTAGTATAT
ATCCTGACGC	AAAAGACTAA	GCTTACTGTA	GTCGCCTTCG	TCATCATATA
310	320	330	340	350
*	*	*	*	*
GCTGCATCGG	CGGCGGCATG	ACTGAATTTT	TCTCGCCGGA	GACTTCGCCG
CGACGTAGCC	GCCGCCGTAC	TGACTTAAAA	AGAGCGGCCT	CTGAAGCGGC
360	370	380	390	400
*	*	*	*	*
GCGGAGATCA	CTTCACTGAA	ACGCCTATCG	GAAACACTGG	AATCTATCTT
CGCCTCTAGT	GAAGTGACTT	TGCGGATAGC	CTTTGTGACC	TTAGATAGAA
410	420	430	440	450
*	*	*	*	*
CGATGCGTCT	TTGCCGGAGT	TTGACTACTT	CGCCGACGCT	AAGCTTGTGG
GCTACGCAGA	AACGGCCTCA	AACTGATGAA	GCGGCTGCGA	TTCAACACCC
460	470	480	490	500
*	*	*	*	*
TTTCCGGCCC	GTGTAAGGAA	ATTCCGGTGC	ACCGGTGCAT	TTTGTCGGCG
AAAGGCCGGG	CACATTCTTT	TAAGGCCACG	TGGCCACGTA	AAACAGCCCG
510	520	530	540	550
*	*	*	*	*
AGGAGTCCGT	TCTTTAAGAA	TTTGTCTCTG	GGTAAAAAGG	AGAAGAATAG
TCCTCAGGCA	AGAAATTCTT	AAACAAGACG	CCATTTTTC	TCTTCTTATC

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560	570	580	590	600
*	*	*	*	*
TAGTAAGGTG	GAATTGAAGG	AGGTGATGAA	AGAGCATGAG	GTGAGCTATG
ATCATTCCAC	CTTAACCTCC	TCCACTACTT	TCTCGTACTC	CACTCGATAC
610	620	630	640	650
*	*	*	*	*
ATGCTGTAAT	GAGTGTATTG	GCTTATTTGT	ATAGTGGTAA	AGTTAGGCCT
TACGACATTA	CTCACATAAC	CGAATAAACA	TATCACCATT	TCAATCCGGA
660	670	680	690	700
*	*	*	*	*
TCACCTAAAG	ATGTGTGTGT	TTGTGTGGAC	AATGACTGCT	CTCATGTGGC
AGTGGATTTT	TACACACACA	AACACACCTG	TTACTGACGA	GAGTACACCG
710	720	730	740	750
*	*	*	*	*
TTGTAGGCCA	GCTGTGGCAT	TCCTGGTTGA	GGTTTTGTAC	ACATCATTTA
AACATCCGGT	CGACACCGTA	AGGACCAACT	CCAAAACATG	TGTAGTAAAT
760	770	780	790	800
*	*	*	*	*
CCTTTCAGAT	CTCTGAATTG	GTTGACAAGT	TTCAGAGACA	CCTACTGGAT
GGAAAGTCTA	GAGACTTAAC	CAACTGTTCA	AAGTCTCTGT	GGATGACCTA
810	820	830	840	850
*	*	*	*	*
ATTCTTGACA	AAACTGCAGC	AGACGATGTA	ATGATGGTTT	TATCTGTTGC
TAAGAAGTGT	TTTGACGTCG	TCTGCTACAT	TACTACCAA	ATAGACAACG
860	870	880	890	900
*	*	*	*	*
AAACATTTGT	GGTAAAGCAT	GCGAGAGATT	GCTTTCAAGC	TGCATTGAGA
TTTGTAATAA	CCATTTTCGT	CGCTCTCTAA	CGAAAGTTCT	ACGTAACTCT
910	920	930	940	950
*	*	*	*	*
TTATTGTCAA	GTCTAATGTT	GATATCATAA	CCCTTGATAA	AGCCTTGCCCT
AATAACAGTT	CAGATTACAA	CTATAGTATT	GGGAAGTATT	TCGGAACGGA
960	970	980	990	1000
*	*	*	*	*
CATGACATTG	TAAAACAAAT	TACTGATTCA	CGAGCGGAAC	TTGGTCTACA
GTAAGTAAAC	ATTTTGTTTA	ATGACTAAGT	GCTCGCCTTG	AACCAGATGT
1010	1020	1030	1040	1050
*	*	*	*	*
AGGGCCTGAA	AGCAACGGTT	TTCTTGATAA	ACATGTTAAG	AGGATACATA
TCCCGGACTT	TCGTTGCCAA	AAGGACTATT	TGTACAATTC	TCCTATGTAT
1060	1070	1080	1090	1100
*	*	*	*	*
GGGCATTGGA	TTCTGATGAT	GTTGAATTAC	TACAAATGTT	GCTAAGAGAG

268080-4880680

CCCGTAACCT	AAGACTACTA	CAACTTAATG	ATGTTTACAA	CGATTCTCTC
1110	1120	1130	1140	1150
*	*	*	*	*
GGGCATACTA	CCCTAGATGA	TGCATATGCT	CTCCATTATG	CTGTAGCGTA
CCCGTATGAT	GGGATCTACT	ACGTATACGA	GAGGTAATAC	GACATCGCAT
1160	1170	1180	1190	1200
*	*	*	*	*
TTGCGATGCA	AAGACTACAG	CAGAACTTCT	AGATCTTGCA	CTTGCTGATA
AACGCTACGT	TTCTGATGTC	GTCTTGAAGA	TCTAGAACGT	GAACGACTAT
1210	1220	1230	1240	1250
*	*	*	*	*
TTAATCATCA	AAATTC AAGG	GGATACACGG	TGCTGCATGT	TGCAGCCATG
AATTAGTAGT	TTTAAGTTCC	CCTATGTGCC	ACGACGTACA	ACGTCGGTAC
1260	1270	1280	1290	1300
*	*	*	*	*
AGGAAAGAGC	CTAAAATTGT	AGTGTCCCTT	TTAACCAAAG	GAGCTAGACC
TCCTTTCTCG	GATTTTAAACA	TCACAGGGAA	AATTGGTTTC	CTCGATCTGG
1310	1320	1330	1340	1350
*	*	*	*	*
TTCTGATCTG	ACATCCGATG	GAAGAAAAGC	ACTTCAAATC	GCCAAGAGGC
AAGACTAGAC	TGTAGGCTAC	CTTCTTTTCG	TGAAGTTTAG	CGGTTCTCCG
1360	1370	1380	1390	1400
*	*	*	*	*
TCACTAGGCT	TGTGGATTTT	AGTAAGTCTC	CGGAGGAAGG	AAAATCTGCT
AGTGATCCGA	ACACCTAAAG	TCATTCAGAG	GCCTCCTTCC	TTTTAGACGA
1410	1420	1430	1440	1450
*	*	*	*	*
TCAATGATC	GGTTATGCAT	TGAGATTCTG	GAGCAAGCAG	AAAGAAGAGA
AGCTTACTAG	CCAATACGTA	ACTCTAAGAC	CTCGTTCGTC	TTTCTTCTCT
1460	1470	1480	1490	1500
*	*	*	*	*
CCCTCTGCTA	GGAGAAGCTT	CTGTATCTCT	TGCTATGGCA	GGCGATGATT
GGGAGACGAT	CCTCTTCGAA	GACATAGAGA	ACGATACCGT	CCGCTACTAA
1510	1520	1530	1540	1550
*	*	*	*	*
TGCGTATGAA	GCTGTTATAC	CTTGAAAATA	GAGTTGGCCT	GGCTAAACTC
ACGCATACTT	CGACAATATG	GAACTTTAT	CTCAACCGGA	CCGATTGAG
1560	1570	1580	1590	1600
*	*	*	*	*
CTTTTTCCAA	TGGAAGCTAA	AGTTGCAATG	GACATTGCTC	AAGTTGATGG
GAAAAAGGTT	ACCTTCGATT	TCAACGTTAC	CTGTAACGAG	TTCAACTACC
1610	1620	1630	1640	1650
*	*	*	*	*

260800-1220000

CACTTCTGAG TTCCCACTGG CTAGCATCGG CAAAAAGATG GCTAATGCAC  
GTGAAGACTC AAGGGTGACC GATCGTAGCC GTTTTCTAC CGATTACGTG

1660 1670 1680 1690 1700  
\* \* \* \* \*

AGAGGACAAC AGTAGATTTG AACGAGGCTC CTTTCAAGAT AAAAGAGGAG  
TCTCCTGTTG TCATCTAAAC TTGCTCCGAG GAAAGTTCTA TTTTCTCCTC

1710 1720 1730 1740 1750  
\* \* \* \* \*

CACTTGAATC GGCTTAGAGC ACTCTCTAGA ACTGTAGAAC TTGGAAAACG  
TGGAACCTTAG CCGAATCTCG TGAGAGATCT TGACATCTTG AACCTTTTGC

1760 1770 1780 1790 1800  
\* \* \* \* \*

CTTCTTTCCA CGTTGTTTCAG AAGTTCATAA TAAGATCATG GATGCTGATG  
GAAGAAAGGT GCAACAAGTC TTCAAGATTT ATTCTAGTAC CTACGACTAC

1810 1820 1830 1840 1850  
\* \* \* \* \*

ACTTGTCTGA GATAGCTTAC ATGGGGAATG ATACGGCAGA AGAGCGTCAA  
TGAACAGACT CTATCGAATG TACCCCTTAC TATGCCGTCT TCTCGCAGTT

1860 1870 1880 1890 1900  
\* \* \* \* \*

CTGAAGAAGC AAAGGTACAT GGAACCTCAA GAAATTCTGA CTAAAGCATT  
GACTTCTTCG TTTCCATGTA CCTTGAAGTT CTTTAAGACT GATTTCGTAA

1910 1920 1930 1940 1950  
\* \* \* \* \*

CACTGAGGAT AAAGAAGAAT ATGATAAGAC TAACAACATC TCCTCATCTT  
GTGACTCCTA TTTCTTCTTA TACTATTCTG ATTGTTGTAG AGGAGTAGAA

1960 1970 1980 1990 2000  
\* \* \* \* \*

GTTCTCTTAC ATCTAAGGGA GTAGATAAGC CCAATAAGCT CCCTTTTAGG  
CAAGGAGATG TAGATTCCCT CATCTATTCTG GGTATTTCGA GGGAAATCC

2010 2020 2030 2040 2050  
\* \* \* \* \*

AAATAGGTAA TTGTATTAGG ATATATGAGG AAGAAGAGGA TTTTCTTGTA  
TTTATCCATT AACATAATCC TATATACTCC TTCTTCTCCT AAAAGAACAT

2060 2070 2080 2090 2100  
\* \* \* \* \*

ACATAGCACT CTTTCCTTTC ATCATTTGAT ATGTCAACAT ACATACAACA  
TGTATCGTGA GAAAGGAAAG TAGTAAACTA TACAGTTGTA TGTATGTTGT

2110 2120 2130 2140 2150  
\* \* \* \* \*

GCTGTACCAT AAAGTTGTAT TGTGCACTT ACAACTTTGA AGAACAGAAT  
CGACATGGTA TTTGAACATA ACAACGTGAA TGTTGAAACT TCTTGTCTTA

2160 2170

2590000-4980000

TTATTTGAAA AAAAAAAAAA AA  
AATAAACTTT TTTTTTTTTT TT

[illegible]

[illegible]

TKAFTEDKEEYDKTNNISSSCSSTSKGVDPKNKLPFRK

FIG. 8A

Dosage effect of NPR1 on Psm ES4326 resistance

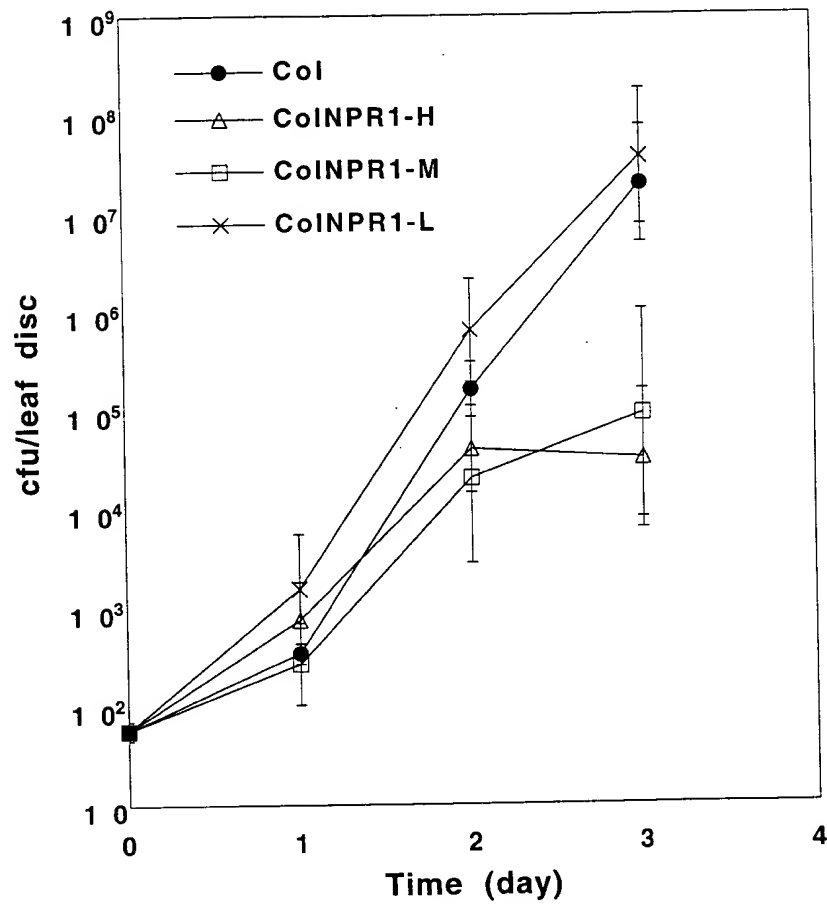
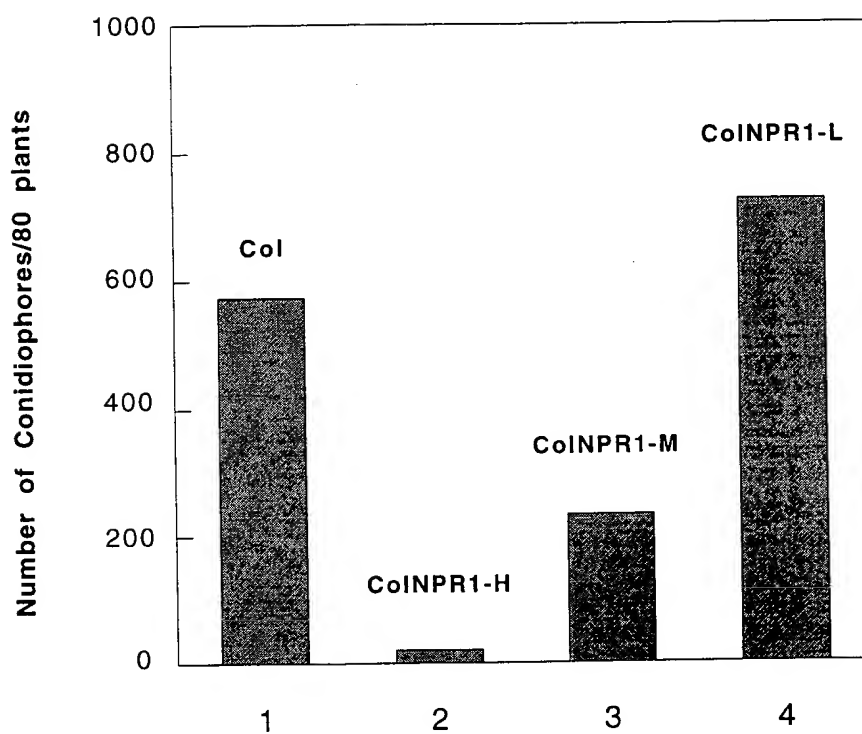


FIG. 8B

Dosage effect of NPR1 on growth of *P. parasitica*



253000-10000000

FIG. 9A

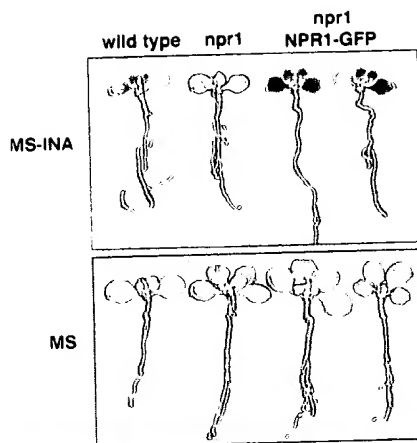


FIG. 9B

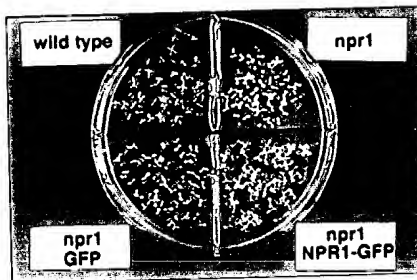


FIG. 9C

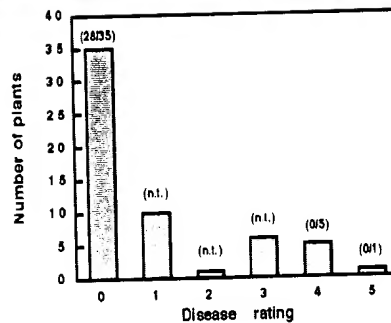
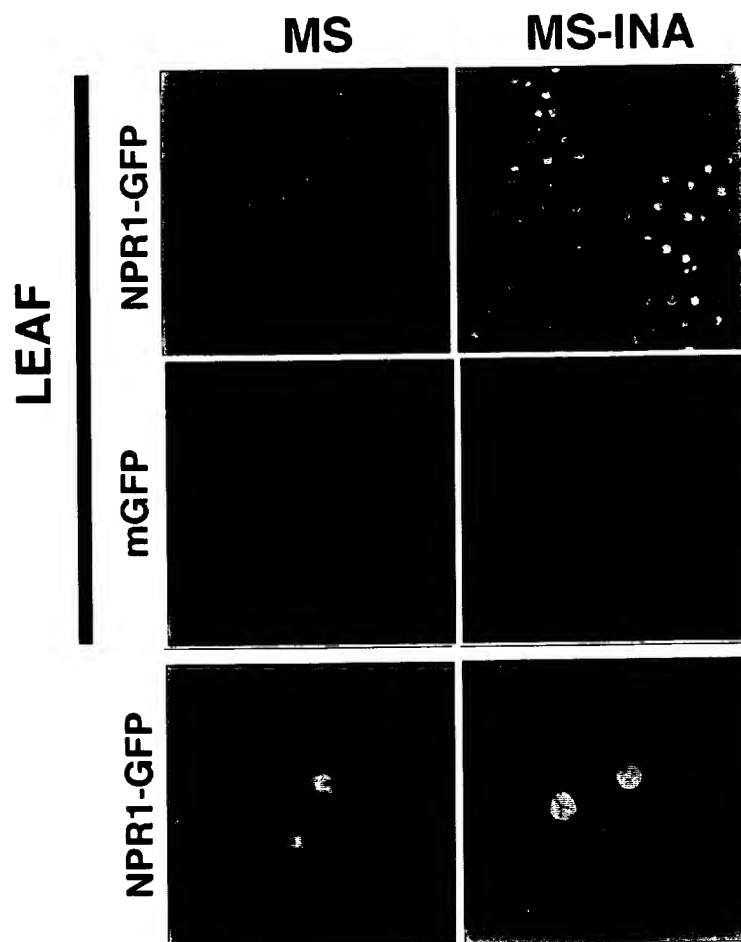




FIG. 10



FIGS. 11A-11G



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